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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: gb_ba1:
2: gb_ba2:
3: gb_in1:
4: gb_in2:
5: gb_in2:
6: gb_in3:
7: gb_om:*
8: gb_ov:*
9: gb_patl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May 14, 2001, 18:24:52; Search time,1113.17 Seconds (without alignments)
225.225 Million cell updates/sec
1283235 seqs, 7373929652 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-373-230-5
17
1 TTYGARGARATGGAYCC 17
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	Score
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MMU66244	ASIGIF	E12010	E11744	E10609	E17139	E14760	E14257	E13264	AR072044	AR072047	ID
Ubb244 Mus Muscuiu			-	EIU609 Mouse CONA	EI/IS MULTING HANG	B14/00 CONA GILCOUT	-		ARO/2044 Sequence	AR072047 Sequence	Description

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RESULT
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Okamura,H., Tanimoto,T., Torigoe,K., Kunikata,T., Tani
Kohno,K. and Kurimoto,M.
Interferon-gamma (IFN-.gamma.) inducing factor (IGIF,
purified from murine liver
Patent: US 5912324-A 5 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                       AR072047
Sequence 5
AR072047
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                                                                                                                                                                                                                                                                                                                               Unclassified.
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AF155773
CEK10C8
                                                                                                    Score 15.4; DB y,
Pred. No. 3.4e+02;
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AC006637
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AF085184
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AF024633
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AB035069
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HS22F01
AC010176
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US 5912324.
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AL109967 Homo sapi
AL109967 Homo sapi
AC010176 Homo sapi
AC010176 Homo sapi
G01707 chicken STS
U39192 Mus musculu
AL143803 Anopheles
AL439404 T7 end of
AL424051 clone AZ0
AF318610 Caenorhab
AF046922 Colletotr
AB035057 Drosophil
AB035066 Drosophil
L36027 Mus musculu
AB035062 Drosophil
AB035062 Drosophil
AB035065 Drosophil
AB035065 Drosophil
AB035065 Drosophil
AF024633 Magnaport
AF015753 Magnaport
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AF015773 Gibberell
Z74474 Caenorhabdi
Z81330 Human DNA s
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Best Local Similarity 76.5%;
Matches 13; Conservative
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244 TTTGAGGAAATGGATCC 260
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1 (bases 1 to 471)
Torigoe, K., Tanimoto, T.,
AGENT FOR SENSITIVE DISE
Patent: JP 1997157180-A
HAYASHIBARA BIOCHEM LAB
OS Mus sp. (mouse)
PN JP 1997157180-A/2
PD 17-JUN-1997
PF 24-JAN-1996 JP 1996(
PR 10-MAR-1995 JP 95P
04-OCT-1995 JP 95P
PI TORIGOE KAKUTT
                                                                                                                                                                                                 PI TORIGOE KAKUJI,
KURIMOTO MASASHI
PC A61K38/00, A61K38
PC C07K14/54,
PC C07K14/55;
                                                                                               Mus sp.
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JP 1997157180-A/2.
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E13264
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AR072044
AR072044.1
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Okamura, H., Tanimoto, T., Torigoe, K., Kunikata, T., Taniguchi, M.,
Kohno, K. and Kurimoto, M.
Interferon-gamma (IFN-.gamma.) inducing factor (IGIF, IL-18)
purified from murine liver
Patent: US 5912324-A 1 15-JUN-1999;
Location/Qualifiers
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topology: Linear;
Feature is identified
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                                       /product='interferon-gamma inducer protein'.
Location/Qualifiers
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/db_xref="taxon:10095"
91 c 92 g
                           organism="Mus sp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 bp DNA
oding a protein that induces to produce
                                                                                                                                            identified by similarity;
Location/Qualifiers
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patent US 5912324.
                                                                                                                                                                                                                                                                                                                                              80-A 2 17-JUN-1997;
LAB INC
                                                                                                                                                                                                                                                                                                                                                                       O,T., Fukuda,S. and Kurimoto,M.
DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Vertebrata; Mammalia; Eutheria; thi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                        18/00,A61K38/00,A61K38/00,A61K38/00,C07K14/52,
                                                                                                                                                                                                                                                                  1996028722
95P 78357, 29-SEP-1995 JP 95P
279906
                                                                                                                                                                                                                                                TANIMOTO TADAO, FUKUDA SHIGEATSU, PI
                                                                               /organism='Mus sp.'
/tissue_type='liver'
1 . .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 9;
Pred. No. 4.5e+02;
4; Mismatches 0
                                                                                                                       .471
 125 t
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1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 -JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                            274988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ORIGIN

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RESULT
E14257
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                                RESULT
E14760
LOCUS
                                                                                                           da
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                                                                                                                                                                                                                                                              BASE COUNT
               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                        source
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244 TTTGAGGAAATGGATCC 260
                                                                                                          244 TTTGAGGAAATGGATCC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 471)

2 Akita,K., Nukada,Y., Fujii,M., Tanimoto,T. and Kurimoto,M.
PROTEIN FOR INDUCING PRODUCTION OF INTERFERON-GAMMA IN

IMMUNOCOMPETENT CELL

Patent: JP 1997289896-A 1 11-NOV-1997;

HAYASHIBARA BIOCHEM LAB INC

OS Mus sp. (mouse)
PN JP 1997289896-A/1

PD 11-NOV-1997

PP 20-SEP-1996 JP 1996269105

PR 26-SEP-1995 JP 95P 270725, 29-FEB-1996 JP 96P 67434 PI

KURIMOTO MASASHI

PC C12P21/02,A61K9/06,A61K38/00,A61K38/00,A61K38/00, PC

A61K38/00.
                                                                                                                                       H
                                                                                                                                      TTYGARGARATGGAYCC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
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E14257
                                                                                                                                                                      <u>, s</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E14257.1 GI:5708940 JP 1997289896-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strandedness:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ЪС
cDNA encoding polypeptide which induces interferon-gamma production \ensuremath{\mathsf{HIGIF}} .
                            E14760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                               162 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                               topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A61K38/00, A61K38/00, C07K14/47, (C12P21/02, C12R1:91); CC
                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                           /organism="Mus sp."
/db_xref="taxon:10095"
91 c 92 g
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double
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                                                                                                                                                                                  90.6%;
                                471 bp
                                                                                                                                                                                                                                                                                                                                          factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 4.5e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                /product='mouse interferon gamma-inducing
or'.
                                                                                                                                                                                                                                                                                                                                                                                  /organism='Mus sp.'
/tissue_type='liver'
                                                                                                                                                                     Score 15.4; DB 10;
Pred. No. 4.5e+02;
1; Mismatches 0;
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                                                                                                                                                                                                  Length 471;
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                                 28-JUL-1999
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SOURCE
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                                                                                                                                                                                           REFERENCE
AUTHORS
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KEYWORDS
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E17139
                                                                                                                                                                                                                                                                         SOURCE
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                                                                                                                                                                                                                                                                                                                           DEFINITION ACCESSION
                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                             TITLE
                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTYGARGARATGGAYCC
                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 471)
Ushio,S., Torigoe,K., Tarinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ushio, S., Torigoe, K., Tanimoto, T., Okamura, H. and Kurimoto, M. POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON-GAMMA Patent: JP 1998007699-A 2 13-JAN-1998; HAYASHIBARA BIOCHEM LAB INC OS Mus sp. (mouse) PN JP 1998007699-A/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E14760
E14760.1 GI:570
JP 1998007699-A,
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 471)
Matthew, T.G., Nicholl, J.H., Udagawa, N. and Kurimoto, M. OSTEOCLAST-FORMATION INHIBITOR Patent: JP 1998236974-A 5 08-SEP-1998; HAYASHIBARA BIOCHEM LAB INC
                                                                                                                                                                                                                                                                                            Murine mRNA for inte
E17139
E17139.1 GI:5711822
JP 1998236974-A/5.
                                                                                                                                                                                                                                                                         Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                           sp.
                                                                              Mus sp. (mouse)
JP 1998236974-A/5
08-SEP-1998
25-FEB-1997 JP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp. (mouse)
JP 1998007699-A/2
13-JAN-1998
13-JAN-1998
18-SEP-1995 JP 1997058547
15-NOV-1994 JP 94P 304203
USHIO SHINPEI, TORIGOE KAKUJI, TANIMOTO TADAO, OKAMURA HARUKI, KURIMOTO MASASHI
C07K14/52,C07H21/04,C12N1/21,C12N15/09,C12P21/02//A61K38/00,(C12N1/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C12R1:19), (C12P21/02, C12R1:19);
          A61K38/00, A61K38/00//C07K14/54, C12N15/09;
strandedness: Double;
                                              08-SEP-1998
25-FEB-1997 JP 1997055468
MATTHEW TODD GALSPIE, NICHOLL JOY HOOWOOD, UDAGAWA NOBUYUKI, KURIMOTO MASASHI
topology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus sp."
/db_xref="taxon:10095"
a 91 c 92 ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Mus sp.'
/tissue_type='liver'.
Location/Qualifiers
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7699-A/2.
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76.5%;
                                                                                                                                                                                                                                                                                                                                           171 bp DNA
c interleukin-18 (IL-18).
  Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .471
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BASE COUNT
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E10609
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                     source
                                                                                                                                                                                     Okamura H., Tanimoto T., Torigoe K., Kurimoto M.; "PROTEIN INDUCING PRODUCTION OF INTERFERON-GAMMA"; Patent number JP1996027189-A/1, 30-JAN-1996. HAYASHIBARA BIOCHEM LAB INC.
                                                                                                                                                                                                                      1-471
                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                          JP 1996027189-A/1.
                                                                                                                                                                                                                                                                                                         08-OCT-1997
02-SEP-2000
                                                                                                                                                                                                                                                                                                                                               E10609;
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                                                     mat_peptide
                                                                           source
                                                                                           Кеу
                                                                                                                 OKAMURA HARUKI, TANIMOTO TADAO, TORIGOE KAKUJI, KURIMOTO MASASHI C07K14/52, A61K38/00, A61K38/00, C12N1/21, C12N15/09, C12P21/02//C07K14/57;
                                                                                                                                              30-JAN-1996
14-JUL-1994 JP 1994184162
                                                                                                                                                                        Mus
                                                                                                  topology:
                                                                                                           strandedness:
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                                                                                                                                                               s sp. (mouse)
1996027189-A/1
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111111111
                                                                                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                  Metazoa;
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                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                        (Rel.
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                                                                                                  Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                b
              Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus sp."
/db_xref="taxon:10095"
                                                                                                                                                                                                                                                                                                        65,
.471
                                                                                                           Double;
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                                                                                                                                                                                                                                          Chordata; Craniata; Ve. Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                         Q
                             production
                                  /product="a protein
interferon-gamma
                                                                                                                                                                                                                                                                                                                                                             RNA;
                                                           /organism="Mus sp."
/tissue_type="liver"
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 c
                                                                                                                                                                                                                                                                                                      Created)
Last updated,
                                                                                                                                                                                                                                                                                        protein involved in interferon-gamma
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                                                                                                                                                                                                                                                                                                                                                                                                    260
                                                     .471
                                                                                                                                                                                                                                                                                                                                                             ROD;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; D
Pred: No. 4.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism='Mus sp.'
/tissue_type='liver'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471
                                                                                                                                                                                                                                                                                                                                                                                                                                e 15.4; DB 10;
No. 4.5e+02;
ismatches 0;
                                                                                                                                                                                                                                                                                                        Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                 Vertebrata;
                                             involved in
                                                                                                                                                                                                                                          Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                          Euteleostomi; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                471;
                                                                                                                                                                                                                                                                                       production.
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                                                                                                                                                                                                                                                  Mammalia;
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RESULT
E11744
ID E1
XX
AC E1
XX
SV E1
XX
OR
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Query Match
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Matches 13
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Best Local S
Matches 13
                                                                                                                 Sequence
                                                                                              Key
                                                                                                                                                                                                                                                                                                                           [1]
1-471
                                                                                                                                                                                                                                                                                        Ushio.S., Torigoe K., Tanimoto T., Okamura H., Kurimoto M.; "POLYPEPTIDE FOR INDUCING PRODUCTION OF INTERFERON-GAMMA"; Patent number JP1996193098-A/1, 30-JUL-1996. HAYASHIBARA BIOCHEM LAB INC.
                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E11744
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                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1997
02-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E11744.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E11744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 471 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 76.1 les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        1996193098-A/1.
                                                                                                                                                          C07K14/52,C07H21/04,C12
C07K7/06,
C07K7/08,(C12N1/21,C12F
Strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                    Mus musculus (mouse)
JP 1996193098-A/1
30-JUL-1996
18-SEP-1995 JP 1995262062
15-NOV-1994 JP 94P 304203
USHIO SHINPEI, TORIGOE KAKUJI, TANIMOTO TADAO, OKAMURA HARUKI, KURIMOTO MASASHI
                                                                                                                                                   Key
                                                                                                                                  source
. Similarity 13; Conser
                                             471
                                                                                                                                                                                                                                                                                                                                                     ; Metazoa;
Rodentia;
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                            BP;
                                                                                                                                                                                                                                                                                                                                          (house mouse)
>tazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
dentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
                                                           /db_xref="t
/organism="
                                                                                               Location/Qu
                                            162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 A;
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                                            Α;
          90.6%
76.5%
                                                                                                               /organ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA;
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4
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                                                            "Mus musculus"
                                                                     taxon:10090*
                                                                                                              nism="Mus musculus"
ue_type="liver"
                                                                                                                                                                                           2R1:19), (C12P21/00, C12R1:19);
                                                                                                                                                                                                           12N1/21,C12N15/09,C12P21/00//A61K38/00,
                                                                                                                                                                                                                                                                                                                                                                                                     which induce mouse interferon-gamma product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 C; 92 G; 125 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "taxon:10095"
="Mus sp."
                                                                                               ualifiers
                                                                                                                                                 ion/Qualifiers
                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROD; 471 BP.
Score 15.4; DB 45; Pred. No. 4.5e+02; 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 45; Pred. No. 4.5e+02; 4; Mismatches 0;
                                           92 G; 125 T;
                                           1 other;
                Length 471;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 471;
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Gaps
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RESULT
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RESULT
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Best Local
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1-471
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP 1996231598-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1997 (Rel. 52, 02-SEP-2000 (Rel. 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E12010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "MONOCLONAL ANTIBODY";
"MONOCLONAL ANTIBODY";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunocompetent cell
                                                                                                                                                                                                Sequence 471 BP; 162 A; 91 C; 92 G; 125 T;
                                                                                                                                                                                                                                                                  source
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||:||:||:||:|||||
244 TTTGAGGAAATGGATCC
                                                 244 TTTGAGGAAATGGATCC 260
                                                                                                                               Local
                                                                                1 TTYGARGARATGGAYCC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (mouse)
JP 1996231598-A/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUNIKATA TOSHIO, TANIGUCHI MUTSUKO, KONO KEIZO, KURIMOTO MASASHI C07K16/24,C07K1/16,C07K1/18,C07K1/22,C07K1/26,C07K1/30, C07K1/34,C12N5/10, C07K1/34,C12N5/10, C12N15/02,C12P21/08,G01N33/53,G01N33/577//A61K38/21,A61K39/395,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear; hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-
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                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; RNA; ROD; 471 BP.
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP1996231598-A/2, 10-SEP-1996.
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                               /db_xref="taxon:10090"
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                    No;
                                                                                                                                                                                                                                                                .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide which introduce interferon-gamma product in
                                                                                                                                90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 /organism="Mus muscu
/tissue_type="liver"
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                                                                                                                                                                                                                                                                                                                                                                    .471
                                                                                                                                Score 15.4;
Pred. No. 4.
                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                  musculus"
                                                                                                                                DB 45;
.5e+02;
                                                                                                                                                                                                    1 other;
                                                                                                                   0;
                                                                                                                                                  Length 471;
                                                                                                                  Indels
                                                                                                                  Gaps
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MMU66244
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                                                                                                                                                                                                                                                                              2 (bases 1 to
Rothe, H., Copeli
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
13; Conser
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Direct Submission

Submitted (21-OCT-1996) H.J. Schluesener, Inst.f. Hirnforschung,

Submitted (21-OCT-1996) H.J.
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synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Direct Submissi
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Y09278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schluesener, H.J
Unpublished
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1 (bases 1 to 471)
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                                                                                                                                                                                                                                                                                                                                                                                                            Rothe, H., Jenkins, N.A., Copeland, N.G. and Kolb, H. Active stage of autoimmune diabetes is associated with the expression of a novel cytokine, IGIF, which is located near Idd2 J. Clin. Invest. 99 (3), 469-474 (1997)
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                                                                                                                                                                                                                        Submitted (06-, Hennekamp 65, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U66244.1
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97174346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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/protein_id="CAA70473.1"
/db_xref="GI:1666284"
/translation="NFGRIHCTTAVIRNINDQVLFVDKRQPVFEDMTDIDQSASEPQT
RLIIYMYKDSEVRGLAVTLSVKDSKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQ
KRVPGHNKMEFESSLYEGHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS"
100 c 130 g 93 t
                                                                                                /organ
/strai
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/db_xref="taxon:32630"
/tissue_type="pancreas"
                             /strain="non obese diabetic (NOD)"
/db_xref="taxon:10090"
/chromosome="9"
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Duesseldorf 40225, Germany
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                                                                                                                              ism="Mus musculus"
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                  13;
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Okamura, H., Tsutui, H., Komatsu, T., Yutsudo, M., Hakura, A., Okamura, T., Torigoe, K., Okura, T., Nukada, Y., Hattori, K., Namba, M., Tanabe, F., Konishi, K., Fukuda, S. and Kurimoto, M. Cloning of a new cytokine that induces IFN-gamma production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse r
D49949
                                                                                                                                                                                                                                                                                                                                                                                     96061009
                                                                                                                                                                                                                                                                                                                                                                                                 Nature 378 (6552), 88-91 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-MAR-1995) to the DDBJ/EMBL/GenBank databases. Haruki Okamura, Hyogo College of Medicine, Department of Bacteriology; Mukogawa 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamura, H.
                                                                                                                                                                                                                                                                                                                                                                                                                  cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGIF precursor polypeptide.
Mus musculus liver cDNA to mRNA, clone pMuGF37B-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                         ρ
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SKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLAC
QKEDDAFKLILKKKDENGDKSVMFTLTNLHQS"
                                                                                                                         966
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SKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLAC
QKEDDAFKLILKKKDENGDKSVISLTNLHQ"
1111 c 113 g 152 t
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                     'organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1064822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi; Muridae; Murinae; Mus. 1 to 866)
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                               90.6%;
76.5%;
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76.5%;
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                           Pred.
                             Score 15.4; DB 94
Pred. No. 4.7e+02;
                                                                                                         187
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                 Mismatches
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4.6e+02;
                                           DB 94;
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                                             866;
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              0;
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               Gaps
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               0;
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SOURCE
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513 TTTGAGGAAATGGATCC
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                            Mammalia;
                                          Eukaryota;
                                                          Homo sapiens
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Corporation (JST) a
Research (RIKEN).
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Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Mar 17, 2000 this sequence version replaced gi:4835598.
Sequence updated (15-Mar-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Yada, Direct Submission Submitted (13-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori, M., Ishii, K., Toyoda, A., Taylor, T.I. Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Homo sapiens 35,143 genomic DNA of 21q21.1. Published Only in DataBase (1999) In press 2 (bases 1 to 35143) Hattori, M., Ishii, K., Toyoda, A., Taylor, T.I. Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Fujiyama, A., Yada, T., Totoki, Y. and Sakaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone:T1539, LL56-APP region, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is a part of the data (ACCESSION No. AP000136 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria
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/map="21q21.1
a 7036 c
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/db_xref="taxon:9606"
/chromosome="21"
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                     Eutheria; P
1 to 59955)
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   Linton, L
                                                                      Metazoa;
                                                                                                                                                                  GI:10280784
                                                                                                                                                                                                                                                            59955 bp
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                                                                                                                                                                                                                             chromosome 4 clone CTD-2353K2 map 4, LOW-PASS SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ect is supported by Japan Science Technology and The Institute of Physical and Chemical
., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
[., Totoki, Y. and Sakaki, Y.
                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Toyoda, A., Taylor, T.D., Hong-Seog, P., Totoki, Y. and Sakaki, Y. genomic DNA of 21q21.1-q21.2
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Bairren,B., Linton,L., Nusbaum,C., Eander,E., Boguslavkiy,L.,

Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,

Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,

DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,

FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,N.

Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,

-Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G.

Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,

McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,

O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K.,

Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,F

Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.

Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 4, clone CTD-2353K2
                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 74 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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Phack.M., Riley,R.,
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20176: gap of
21013: contig of 640 bp
1113: gap of
21013: contig of 737 bp in length
11213: gap of
21872: contig of 759 bp
112634: contig of 662 bp in length
22634: contig of 662 bp in length
2340: gap of
24159: contig of 719 bp in length
24993: contig of 719 bp in length
2503: gap of
26519: gap of
26519: gap of
27253: contig of 634 bp in length
28058: contig of 634 bp in length
28058: gap of
28058: contig of 664 bp in length
29594: contig of 676 bp in length
30458: contig of 676 bp in length
30458: contig of 676 bp in length
31323: contig of 764 bp in length
31323: gap of
31323: contig of 767 bp
31323: gap of
330451: gap of
3304527: contig of 690 bp in length
34637: contig of 648 bp in length
5721: gap of
3723: gap of
3724: gap of
3724: gap of
38624: contig of 788 bp in length
100 bp
3724: gap of
38624: contig of 788 bp in length
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3133: gap of
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3136: gap of
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11203: contig of 624
13: gap of 100
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9: gap of 100 bp
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2043: c
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1846: contig of 703 bp in
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REFERENCE
AUTHORS
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Locus
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 95155)
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Homo sapiens 12 BAC RP11-407P10 (Rosw
Human BAC Library) complete sequence.
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40427;
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44462: 7
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46891: co
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4: gap of

43747:
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contig of 705 bp:
ap of 100 bp:
contig of 626 bp:
ap of 100 bp:
contig of 617 bp:
ap of 100 bp:
contig of 775 bp:
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gap of 100 bp

i: contig of 753 bp i

gap of 100 bp

i: contig of 615 bp i

gap of 100 bp

i: contig of 635 bp i

gap of 100 bp

i: contig of 737 bp i

gap of 100 bp

i: contig of 757 bp i
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19 of 772 bp
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Catarrhini; Hominidae;
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JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

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Hodgson, A., Hogues, M., Holloway, C., Hollins, E., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martindale, A., Martinez, E., Marondel, I., Martin, R., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Minchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newtson, J., Newtson, N.,
entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and and and of the Features listing.
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                                                                                                                                                                                                                                                                                                                                Submitted (01-JAN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 1, 2001 this sequence version replaced gi:12000225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 95)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                 INFORMATION: http://
gc-help@bcm.tmc.edu
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Direct Submission
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Peery, J., Perez, L.,
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                                                                                                                                                                                                                                                                                               sequence version replaced gi:12000225/www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3., Hamilton, K., Han, J., Harris, C., Ha
Hawes, A., Hernandez, J., Hernandez, O.,
M., Holloway, C., Hollins, B., Homsi, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen, N., Nickerson, E., Nwokenkwo, S., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peters, L., Pickens, R., Primus, E., Pu, L.L., ives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
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COMMENT

REFERENCE AUTHORS

TITLE JOURNAL

В

VERSION

ANNOTATION OF FEATURES:

of a local STSs are database identified using ePCR (Genome Res. 7:541-550) searches latabase that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ double ERAGE: Sequencing is completed to a minimum strand coverage with a minimum of 2 clones and 2

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reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10.000 bases.

QUALSTAT-REPORT

Ore Kuttob	83	82	81	80	79	78	77	76	75	74	73	72	71	70	69	68	67	. 66	65	64	63	62	61	60	59	58	57	56	ភូ	54	53	52	51	50	49	
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Qy 1 TTYGARGARATGGAYCC 17 ||:||:||:||:||:|| Db 69860 TTTGAAGAGATGGATCC 69844 Query Match 90.6%; Score 15.4; DB 88; Length 95155; Best Local Similarity 76.5%; Pred. No. 7.1e+02; Matches 13; Conservative 4; Mismatches 0; Indels 0; 0; Gaps

0;

Search completed: May 14, Job time: 2709 sec 2001, 19:10:01

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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GenEmbl:*
1: gb_bal:*
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5: gb_in2:*
6: gb_in3:*
9: gb_pat1:*
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11: gb_pat2:*
12: gb_pl1:*
13: gb_pl1:*
14: gb_pl1:*
15: gb_pl4:*
16: em_bal:*
9: em_htgo_hum:*
9: em_htgo_inv:*
10: em_htg_hum1:*
11: em_htg_hum2:*
12: em_htg_hum1:*
13: em_htg_hum2:*
14: em_htg_hum3:*
15: em_htg_hum6:*
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17
1 TTYGARGARATGGA
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		ery	בי	DB	ID	scrip
1	٠ ١	90.6	17	9	AR072047	AR072047 Sequence
Ν	•		471	9	AR072044	AR072044 Sequence
ω	15.4	90.6	471	10	E13264	E13264 Mouse cDNA
4	•	•	471	10	E14257	E14257 cDNA encodi
ហ	•	•	471	10	E14760	E14760 cDNA encodi
6	•	90.6	471	10	E17139	E17139 Murine mRNA
7	•	90.6	471	45	E10609	E10609 Mouse cDNA
8	•	90.6	471	4 5	E11744	E11744 cDNA encodi
9	•	90.6	471	45	E12010	E12010 cDNA encodi
10	15.4	90.6	471	56	ASIGIF	Y09278 Artificial
11	15.4	90.6	572	94	MMU66244	U66244 Mus musculu

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RESULT
AR072047
RESULT
AR072044
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Okamura, H., Tanimoto, T., Torigoe, K., Kunikata, T., Taniguchi, M., Kohno, K. and Kurimoto, M.
Interferon-gamma (IFN-.gamma.) inducing factor (IGIF, IL-18) purified from murine liver
Patent: US 5912324-A 5 15-JUN-1999;
Location/Qualifiers
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pred. No. 3.4e+02;
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                                                          ...AR-1995 JP 95P 78357, 29-SEP-1995 JP 95P 274988, PR
...OCT-1995 JP 95P 279906
PI TORIGOE KAKUJI, TANIMOTO TADAO, FUKUDA SHIGEATSU, PI
KURIMOTO MASASHI
PC A61K38/00,A61K38/00,A61K38/00,A61K38/00,C07K14/52,
PC C07K14/54,
PC C07K14/55;
CC strandedness: Double;
CC topology: Linear;
CC feature is identified by similarity:
FH Key Location/Qualifier
FT source 1...477
FT mat -
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E13264.1 GI:325
JP 1997157180-A/
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1 (bases 1 to 471)
Torigoe, K., Tanimoto, T., Fukuda, S. and Kurimoto, M. .

AGENT FOR SENSITIVE DISEASE
Patent: JP 1997157180-A 2 17-JUN-1997;
HAYASHIBARA BIOCHEM LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E13264 471 bp DNA PA3 Mouse cDNA encoding a protein that induces interferon-gamma.
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Interferon-gamma (IFN-.gamma.) inducing factor (IGIF, IL-18)
purified from murine liver
Patent: US 5912324-A 1 15-JUN-1999;
Location/Qualifiers
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7180-A/2.
                                                 /product='interferon-gamma inducer protein'.
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Pred. No. 4.5e+02;
4; Mismatches 0;
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    1 others
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0;

ORIGIN

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RESULT 4
E14257
LOCUS
DEFINITION
ACCESSION
                                       RESULT
E14760
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SOURCE
             DEFINITION
                           LOCUS
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                                                                                                                                                                  Best
                                                                                                                                                       Matches
                                                                                                                                                                               Query Match
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Best Local
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                                                                                                                                                                                                                                        COUNT
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                                                                                                244
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                                                                                           TTTGAGGAAATGGATCC 260
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                                                                                                                                                   l Similarity 76.
13; Conservative
            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OS Mus sp. (mouse)
PN JP 1997289896-A/1
PD 11-NOV-1997
PF 20-SEP-1996 JP 1996269105
PR 26-SEP-1995 JP 95P 270725, 29-FEB-1996 JP 96P 67434 PI
AKITA KENJI, NUKADA YOSHIYUKI, FUJII MITSUKIYO, TANIMOTO TADAO, PI
KURIMOTO MASASHI
PC C12P21/02,A61K9/06,A61K38/00,A61K38/00,A61K38/00, PC
HIGIF
                       E14760
                                                                                                                                                                                                                                                                                                                                                                                                                                      strandedness: Double; CC topology: Linear CC hypothetical: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: JP 1997289896-A 1 11-NOV-1997;
HAYASHIBARA BIOCHEM LAB INC
OS Mus sp. (mouse)
PN JP 1997289896-A/1
PD 11-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 471)
1 (bases 1 to 471)
Akita, K., Nukada, Y., Fujii, M., Tanimoto, T. and Kurimoto, M. PROTEIN FOR INDUCING PRODUCTION OF INTERFERON-GAMMA IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNOCOMPETENT CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A61K38/00,
                                                                                                                                                                                                                                         162
         encoding polypeptide which induces
                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A61K38/00, A61K38/00, C07K14/47, (C12P21/02, C12R1:91); CC
                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                         anti-sense:
                                                                                                                                                                                                                                                                                                                                                                                                                                      topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                    /organism="Mus sp."
/db_xref="taxon:10095"
91 c 92 g
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                        471 bp
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                                                                                             260
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                                                                                                                                                                                                                                                                                                            factor'
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/tissue_type='liver'
1. .471
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        /product='mouse interferon gamma-inducing
                                                                                                                                                                Score 15.4;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 10;
Pred. No. 4.5e+02;
; Mismatches 0;
                         DNA
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                                                                                                                                                    Mismatches
                                                                                                                                                              No.
                                                                                                                                                                                                                                        125
                                                                                                                                                  4; DB 10;
4.5e+02;
ches 0;
     interferon-gamma production
                                                                                                                                                   Indels
                                                                                                                                                                            Length 471;
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                       28-JUL-1999
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__yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom .ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Muridae; Musass I to 471)

L.JRS Ushio, S., Torigoe, K., Tanimoto, T., Okamura, H. and Kurimoto, M. PolyPepride Inductor Ropouction of INTERPERON-GAMMA Patent: JP 1998007699- A: 21 3-JAN-1998;

HAYASHIBARA BIOCHEM LAB INC

COMMENT OSI ON 1994 A: 29 197058547
PN JP 198007699- A: 21 3-JAN-1998;
PF 15-NOV-1994 JP 94P 304203
PF 15-NOV-1994 JP 94P 304203
PF 16-NOV-1994 JP 94P 304203
PF CCONTAL/21, COTHEL, TORIGOE KAKUJI
PC COTRAL/25, COTHEL, TORIGOE KAKUJI
PC COTRAL/25, COTHEL, OLD COTTEN COTTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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E17139
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ORIGIN
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                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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Best Local Similarity
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Matthew,T.G., Nicholl,J.H., Udagawa,N. and Kurimoto,M. OSTEOCLAST-FORMATION INHIBITOR Patent: JP 1998236974-A 5 08-SEP-1998; HAYASHIBARA BIOCHEM LAB INC OS Mus sp. (mouse) PN JP 1998236974-A/5
PD 08-SEP-1998
PF 25-FEB-1997 JP 1997055468

PF 25-FEB-1997 JP 1997055468
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                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp. .
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Murine
E17139
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JP 1998236974-A/5.
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Mus sp. (mouse)
JP 1998007699-A/2
13-JAN-1998
18-SEP-1995 JP 1997058547
15-NOV-1994 JP 94P 304203
15-NOV-1994 JP 94P 304203, TANIMOTO TADAO, OKAMURA HARUKI,
                                               KURIMOTO MASASHI
A61K38/00,A61K38/00//C07K14/54,C12N15/09;
                                                                                               MATTHEW TODD GALSPIE, NICHOLL JOY HOOWOOD, UDAGAWA NOBUYUKI,
topology: Linear;
                           strandedness:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/db_xref=":
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/tissue_type='liver'
Location/Qualifiers
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"taxon:10095"
92 g 1
                          Double;
                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 10; Pred. No. 4.5e+02;
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BASE COUNT
ORIGIN
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E10609
ID E1
XX
AC E1
XX
E1
XX
AC E1
XX
OR
DT 08
DT 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E10609
                                                                                                                                                                                                                                                                                                                                                                              Mouse cDNA encoding a protein involved in interferon-gamma production.
                                                                                                                                                                                                                                                                                                                                                                                                                                E10609.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E10609;
                                                                                                                                                                                                                                            Okamura H., Tanimoto T., Torigoe K., Kurimoto M.; "PROTEIN INDUCING PRODUCTION OF INTERFERON-GAMMA"; Patent number JP1996027189-A/1, 30-JAN-1996. HAYASHIBARA BIOCHEM LAB INC.
                                                                                                                                                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                                                                                                                                                            JP 1996027189-A/1.
                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                      1-471
source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTYGARGARATGGAYCC 17
                                                                                                                                       Mus sp. (mouse)
JP 1996027189-A/1
30-JAN-1996
14-JUL-1994 JP 1994184162
OKAMURA HARUKI, TANIMOTO TADAO, TORIGOE KAKUJI,
KURIMOTO MASASHI
C07K14/52,A61K38/00,A61K38/00,C12N1/21,C12N15/09,
C12P21/02//C07K14/57;
strandedness: Double;
                                                                      mat_peptide
                                                                                                    source
                                                                                                                                 topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                  ; Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; RNA; ROD; 471 BP.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus sp."
/db_xref="taxon:10095"
91 c 92 g
                     Location/Qualifiers
  .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%;
                                      /product="a protein involved in
interferon-gamma
production"
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last updated, Version 2)
                                                                           /organism="Mus sp."
/tissue_type="liver"
| ^71
                                                                                                      .471
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/tissue_type='liver'
1..471
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Pred. No. 4.5e+02;
; Mismatches 0
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                                                                                                                                                                                                                                                                                                                      Mus.
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E11744
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Query Match
Best Local
Query Match
Best Local Similarity
Matches 13; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding polypeptide which induce mouse interferon-gamma product.
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                                                                              Sequence 471 BP; 162 A;
                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                     Mus musculus (mouse)

JP 1996193098-A/1

30-JUL-1996

18-SEP-1995 JP 1995262062

15-NOV-1994 JP 94P 304203

USHIO SHINPEI, TORIGOE KAKUJI, TANIMOTO TADAO, OKAMURA HARUKI, KURIMOTO MASASHI
C07K14/52,C07H21/04,C12N1/21,C12N15/09,C12P21/00//A61K38/00,C07K7/08,(C12N1/21,C12R1:19),(C12P21/00,C12R1:19);
                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                           anti-sense:
                                                                                                                                                                                                                                                                                                       topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                         strandedness:
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13; Conser
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus sp.
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                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                NO
                                                                                                             /organism="Mus musculus"
                                                                                                                                Jap_
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                                                                                                                                                                                                                                                                                                            NO;
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                                                                                                                                                                                                                                                                                                                                              Double;
                                                                                                                               _xref="taxon:10090"
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                 90.6%;
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Last updated, Version 2)
                                                                                                                                                                                                            /organism="Mus musculus"
/tissue_type="liver"
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                                                                                 91 C; 92 G; 125 T; 1 other;
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Pred. No. 4.5e+02;
4; Mismatches 0;
Score 15.4; DB 45;
Pred. No. 4.5e+02;
4; Mismatches 0;
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                                  Length 471;
    Indels
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Best Local Similarity
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1-471
Kunikata T., Taniguchi M., Kono
"MONOCLONAL ANTIBODY";
Patent number JP1996231598-A/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAYASHIBARA BIOCHEM LAB INC
                                                       244
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244 TTTGAGGAAATGGATCC
10
                                                                                        1 TTYGARGARATGGAYCC
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TTTGAGGAAATGGATCC
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JP 1996231598-A/2
10-SEP-1996
23-FEB-1995 JP 199505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KURIMOTO MASASHI
C07K16/24,C07K1/16,C07K1/18,C07K1/22,C07K1/26,C07K1/30,
C07K1/34,C12N5/10,
C12N15/02,C12P21/08,G01N33/53,G01N33/577//A61K38/21,A61K39/395,
(C12P21/08,
C12R1:91);
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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/organism="Mus musculu
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), TANIGUCHI MUTSUKO,
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76.5%;
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/tissue_type="liver"
                                                     260
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4.5e+02;
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ae; Murinae;
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                                TITLE
                                                                                                                   JOURNAL
                                                                                                                                              AUTHORS
                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                         source
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244 TTCGAAGAAATGGACCC 26
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                                                                                                                                                                                                                                                                                                                                 Mus musculus
U66244
U66244.1 GI:
                                                                                             Direct Submission
Submitted (06-AUG-1996) Diabetes Research Institute,
Hennekamp 65, Duesseldorf 40225, Germany
                                                                                                                                                                         J. Clin. Invest. 97174346
                                                                                                                                                                                                   Rothe, H., Jenkins, N.A
Active stage of autoir
expression of a novel
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                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; M
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                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                              MMU66244
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Location/Qualifiers
1. .471
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Submitted (21-OCT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schluesener, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic artificial
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Y09278
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he, H., Copeland, N
                                                                                                                                                                                                                                               (bases
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/codon_start=1
/transl_table=11
                                                                                    Location/Qualifiers
            /organism="Mus musculus"
/strain="non obese diabetic (NOD)"
/db_xref="taxon:10090"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="mouse cytokine interferon-gamma inducing factor"
/protein_id="CAA70473.1"
/db_xref="GI:1666284"
/translation="NFGRLHCTTAVIRNINDQVLFVDKRQPVFEDMTDIDQSASEPQT
RLIIYMYKDSEVRGLAVTLSVKDSKMSTLSCKNKIISFEEMDPPENIDDIQSDLIFFQ
KRVPGHNKMEFESSLYEGHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS"
100 c 130 g 93 t
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_type="pancreas"
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27 Q
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                                                                                                                                                                                     A., Copeland, N.G. and Kolb, H.
immune diabetes is associated with the
cytokine, IGIF, which is located near Idd2
(3), 469-474 (1997)
                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                           .G. and Kolb, H.
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Pred. No. 4.5e+02;
4; Mismatches 0;
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349 TTTGAGGAAATGGATCC 365
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D49949.1 GI:1064822
IGIF precursor polypeptide.
Mus musculus liver cDNA to mRNA, clone pMuGF37B-5.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 866)
2 (bases 1 to 866)
Okamura, H., Tsutui, H., Komatsu, T., Yutsudo, M., Hakura, A.,
Tanimoto, T., Torigoe, K., Okura, T., Nukada, Y., Hattori, K., Akita, K.,
Namba, M., Tanabe, F., Konishi, K., Fukuda, S. and Kurimoto, M.
Cloning of a new cytokine that induces IFN-gamma production by T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 866)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (29-MAR-1995) to the DDBJ/EMBL/GenBank databases. Haruki Submitted (29-MAR-1995) to the DDBJ/EMBL/GenBank databases. Haruki Okamura, Hyogo College of Medicine, Department of Bacteriology;
Mukogawa 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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mRNA for IGIF precursor polypeptide, complete
                                 Conservative
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AVIRNINGENGLESDNFGRLHCTT
AVIRNINGENGLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus'
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                                                                   90.6%;
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bred. No. 4.6e+02;
                                                                   Score 15.4; DB 94; Pred. No. 4.7e+02;
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LL56-APP region AP000229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y. Direct Submission

Direct Submission

Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases.

Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 (Fixen), Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/. Tel:81-42-778-9923, Fax:81-42-778-9924)

On Mar 17, 2000 this sequence version replaced gi:4835598. Sequence updated (15-Mar-2000)
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13; Conser
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                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 4 clone CTD-2353K2 map 4, LOW-PASS SEQUENCE AC080029
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Mammalia; ]
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/db_xref="taxon:9606"
/chromosome="21"
/clone="T1539"
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  Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 project is supported by Japan Science Technology and The Institute of Physical and Chemical
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RESULT 1;

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DEFINITION ACCESSION

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Matches Query Match Best Local

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JOURNAL REFERENCE
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Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G.,
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Direct, Submission
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Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Unpublished
2 (bases 1 to 59955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10743
Center clone name: 2353_K_2
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95155)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Bowie,S., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,(Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Da
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REFERENCE AUTHORS

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Gunarathe, P., Hale, S., Hamilton, K., Han, J., Halis, C., Harti, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L., C., Liu, Y., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., C., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., C., Liu, J., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., C., Marinez, E., Marondel, I., Martin, R., Luna, R., Martin, R., Martinez, E., Marondel, I., Martin, R., Luna, R., Martin, R., Marondel, I., Martin, R., Miner, G., Medor, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Medor, M., Mitchell, T., Mohabbat, K., Montgomery, K.T., McLeod, M.P., Moyayen, N., Neal, C., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Newtson, N., Oyuh, M., Okwuonu, G., Oragunye, N., Oyledo, R., Pace, A., Payton, B., Perery, J., Peters, L., Pickens, R., Primus, E., Pu, L., L., Petery, J., Pickens, R., Primus, E., Pu, L., L., Rolfe, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Scott, G., Shen, H., Shim, C., Shott, G., Shen, H., Shim, C., Shott, G., Shen, H., Shim, C., Shen, H., Shim,
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Elhaj,C., Emerl
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                                                                                                                                                                                                                                                                                                           Submitted (13-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
a,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Emerling,S., Escotto,M., Falls,T., Ferraguto,D.,
Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J.,
Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W.,
P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K.,
P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K.,
                                   AN-2001) Human Genome Sequencing Center, Department d Human Genetics, Baylor College of Medicine, One louston, TX 77030, USA
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COMMENT

Baylor On Jan gc-help@bcm.tmc INFORMATION:)1 this sequence version replaced gi:12000225 http://www.hgsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listin

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and

of a local data local mapping e Repeats a unpublished. are efforts identified using RepeatMasker (A. Smit and P. Green or Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double SEQUENCING READ COVERAGE: Sequencing is completed to a minimum ple strand coverage with a minimum of 2 clones strand clones and 2

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2 (bases 1 to 100000)
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Fujiyama, A., Yada, T., To
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78752 TTTGAGGAAATGGATCC 78736
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                                      TTYGARGARATGGAYCC 17
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                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in DataBase (2000) In press 2 (bases 1 to 100634)
2 (bases 1 to 100634)
2 himizu, N., Kudoh, J. and Shibuya, K.
Direct Submission
Submitted (04-APR-2000) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP001594 100634 bp DNA
Homo sapiens genomic DNA, chromosome (APP-D21S292 region, complete sequence
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1 (bases 1 to 100634)
Shimizu, N., Kudoh, J. and Shibuya, K.
Homo sapiens genomic DNA, chromosome 21, clone:KB580H10,
APP-D21S292 region
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18848 c 2
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e-PCR (Schuler)
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Max-Planck-Institut fuer Molekulare believe.

Max-Planck-Institut fuer Molekulare believe.

Ihnestrasse 73, D-14195 Berlin-Dahlem, Germany
Ihnestrasse 74, D-14195
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> Mzef (Zhang)
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GBF, Dept. of Genome
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BLASTN 2.0.9 (1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      feature lines that evidence is not experimental. PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-At Weg 1, D-38124 F
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Hornischer, K., Loehnert, T.H., Scharfe, M., Schoen, O., Yaspo, M.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                    Minimum score: 60; Minimum identity: 90 %;

'Tandem Repeats': GDE 2.2 option 'tandem'

Minimum length 2 bp; Maximum length 20 bp; Score threshold

Treat N's as mismatches? YES; Allow uniform consensi? NO >

'Inverted Repeats': GDE 2.2 option 'inverted'

'Micro Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG

Islands': GDE 2.2 option 'cpg'

Islands': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                                                                                                                                                                                   Minimum score: 60; Minimum identity: 90 %; 3SSs': BLASTN 2.0.9 (Altschul et al.) Database(s): * embl (GSS), Vers. 60 (16-SE emblnew (GSS), Vers. 60+ (21-NOV-1999).
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           Margin:
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natrix: vertebrate; Minimum score: 0
{u et al.), Vers. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probability: 0.04; Overlapping number: 0 > Xpound (Thomas
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1999
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(Altschul_et al.)
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                                                                               region size 100 bp;
contents 50 %; Observed/Expected 0.6 > 'STS Scan':
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Braunschweig, Germany, E-mail: hornischer@gbf.de,
, bloecker@gbf.de
this sequence version replaced gi:5763708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * RepBase (human), released 22-DEC-1995 (primate), released 22-DEC-1995 . Minimum score 70 %;
              Number of mismatches allowed: 0; Word size: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-38124 Braunschweig, Germany
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Vers. 60+ (21-NOV-1999) . Using
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/note="MZEF prediction, score = complement(1174. .1491)
/note="match: EST Z43821"
complement(1304. .1353)
/note="MZEF prediction, score = 1587. .1627
/note="GRAIL, score = 719.70
 /note="GENSCAN prediction, s
complement(3474. .3530)
/note="GRAIL, score = 94%, c
complement(3894. .4140)
/note="GENSCAN prediction, s
                                                                                                                                                                                                                                                                                                                                      /note="Genefinder prediction" complement(2769. 2880) /note="Genefinder prediction" 2811. 2904
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                                                                   /note="match: EST AA931442"
complement((3471.3489)..(3597.3657))
/note="match: ESTs AA114221 AL042549 Z84022"
complement(3474..4166)
/note="Genefinder prediction"
complement(3474..3675)
                                                                                                                                                                                                       /note="XPOUND prediction,
3423. .3961
                                                                                                                                                                                                                                                                                                3009. .3024
/note="CTC r
                                                                                                                                                                                3442.
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                                                                                                                                                    /note="Genefinder prediction"
3470. .3586
                                                                                                                                                                                                                                                       /note="Genefinder prediction" complement(3213. .3386)
                                                                                                                                                                                                                                                                                                                                                                                         2486. .4115
/note="CpG_island (%GC=69.4, o/e=0.89, 2566. .2933
                                                                                                                                        /note="match:
                                                                                                                                                                                                                                   3321.
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/note="Genefinder prediction"
complement(2478. .2615)
/note="Genefinder prediction"
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/note="XPOUND prediction, score
complement(2133. .2214)
/note="XPOUND prediction, score
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complement(1073..1207)
/note="GENSCAN prediction,
complement(1075..1165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(620. .787)
/note="GRAIL, score = 54%,
complement(620. .739)
/note="GENSCAN prediction,
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/note="XPOUND prediction, score
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1007. .1027
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/chromosome="21"
/clone="""
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AC010176/c
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Best Local Similarity
Matches 13; Conserv
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5074. .5
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/note="GRA]
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/note="96%
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                                                                                                                                                                                                                 complement(8565...8745)
/note="match: GSS B76378"
complement(8759...9069)
/note="match: GSS B76378"
                                                                                                                                                                                                                                                                                                                                                                  complement
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/note="XPOU
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/note="IR1,
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                                                                                                                                                                                                                                                                      /note="XPO
                                                                                                                                                                                                                                                                                               complement(8156. .8185)
/note="match: EST AW002649"
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/note="CpG_
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/note="XPOUND prediction, score = 0.424"
complement(4737. .4843)
/note="Genefinder prediction; GRAIL, score
                                                                                                                                                                                                                                                                                                                          note="mat
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/rpt_family="AluSx"
complement(5436. .5700)
/note="85% identity: matches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="100
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atch: EST AW138710"

at(7474. .7507)

atch: GSS AQ895571"

at(7663. .7737)

EEF prediction, score at(7828. .7903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6% identity: matches 37. .
ily="AluSb"
|13
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it(7161. .7395)

0% identit
                e
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                                                                                                                                                                                                                                                                    UND prediction, score
                                                                                                                                                                                                                                                                                                                        ch: EST AI034376"
                                                                                                                                                                                                                                                                                                                                                                              y="MLTb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (7396. .763)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (5873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , 90% complementary to IR1'
                          DNA PRI 19-SEP-2000 RP11-711K1 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                   ((8134.8154). .(8183.8194))
ch: GSSs AQ080344 AF057094"
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/="MLTb"
                                                                                                                                                                                                                                                                                                                                                                                    identity: matches 23. .99 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   island (%GC=60.4, o/e=0.90, #CpGs=18)"
             sequence
                                                                                                                                                             Score 15.4; DB 91;
Pred. No. 7.3e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley,K.C.
Direct Submission
Submitted (15-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 202103)
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., 
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-SEP-2000) Human Genome Sequencing Center, Depail of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Sep 19, 2000 this sequence version replaced g1:9887569. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res.
of a local database that includes entries from 7:541-550) searches

of a local database t local mapping efforts from dbSTS, GDB,

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. Repeats are identified using RepeatMasker (A. Smit and P. Green

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for SEQUENCING READ annotation region does Low Coverage COVERAGE: Sequencing is completed to meet this standard, it will be indicated in the a minimum

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. ntml.

QUALSTAT - REPORT

Number of N's in consensus :	Number of consensus changing edits:	Fraction of Phrap values less than 40:	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
0	29	0.0287005	9.77954e-05	201669		

73861 89489 89496 89499 39928 45888 54727 54740 73838 Position 139861 200566 ccttctccag(n)gtcagcaatg gagccgagat(t)ccgccactgc acatgagggt(n)gtcaatcttt agaaagggca(n)cattaaaatc tacattgatt(n)tgtatcntan
attntgtatc(n)tannactttg aaancaaaaa(n)gaaaaaaaaa atctgcttgg(n)taaatttatt aaaatctgtg(n)ccttccctgg agagggcaat(n)tatagcacta taatctcttt(n)catgcatttc aaatacagaa(n)caaggaggcc ccctcnct(a)tnccntccccccctcctcnctat(n)ccntccccct ccctccctc(n)ctatnccntc ctcccacccn(n)tcccttgac ţ ţg. ntgtatcnta(n)nactttgctg aagaaagaat(n)caaaaatctg aagagcaaac(n)cattcaaaag attgaaacaa(n)cttcccatgt Original+Context .ctcccaaa(n)ctatccctcc tatcntan(n)actttgctga ttttattg(n)gtctatttaa taaataaa(n)caaaaangaa tccccct(n)cccaccacag acatgagggt(t)gtcaatcttt
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aagaaagaat(a)caaaaatctg aagagcaaac(a)cattcaaaag agagggcaat(t)tatagcacta attgaaacaa(a)cttcccatgt gctgccctta(a)tctcatgtcc tecetetece(e)tececettee ccctccctct(c)ccctcccct Edited+Context

Distribution of Quality < 40 Bases

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Hattori, M., Fujiyama, A., Taylor, T.D.,
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                            Homo sapiens DNA.
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6759. .6947
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/db_xref="taxon:9606"
/chromosome="12"
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                       Chordata;
Primates;
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                       Hominidae; Homo.
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Hattori,M., ruj-i
Park,H.S., Toyoda,A.,
Chki,M., Takagi,T., Sa
Chki,M., Takagi,T., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 30, 2000 this sequence version replaced gi:7717293. The chromosome 21 mapping and sequencing consortium consisting * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gsc.riken.go.jp * URL: http://hgp.gsc.riken.go.jp/
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info.genome@gbf.de
* URL: http://genome.gbf.de/
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* e.mail: nshimizu@dmb-med.keio.ac.jp
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Submitted (10-APR-2
Chromosome 21 Mappi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * e.mail: gscj-subm
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Patterson, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohki, M., Takagi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innestrasse 73, D-14195 Berlin, Germenail: info-chr21@molgen.mpg.de
URL: http://chr21.rz-berlin.mpg.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GBF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute of Molecular Biotechnology, Genome Analysis, eutenbergstrasse 11, D-07745 Jena, Germany, e.mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Max-Planck Institute Ihnestrasse 73, D-141
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30, 2000 this
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                                                                           complement(1021. .1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., akagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., D., Reichwald, K., Rump, A., Schillhabel, M. and Schudy, A., quence of human chromosome 21. The chromosome 21 mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Genome Analysis,
family-"LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Schudy, A., Kawasaki, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soeda, E.,
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AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                        ACCESSION
VERSION
                                                                                                                                                                                                                                                                                        RESULT
G01707
                                                                                                                                                                                                                                                                                                                                                     Db 273372 TTTGAGGAAATGGATCC
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                                                                                                                                                                                                               355 bp
chicken STS ADL288.
G01707
G01707.1 GI:595221
                                             Cheng, H.H.
Unpublished (1994)
Synonyms: B407
Contact: Hans H. Che
Avian Disease and Or
                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                      STS sequence; primer; sequence tagged site. chicken vector=pBluescript II KS+ host=E. coli.
3606 E. Mount Hope Rd, East Lansing, MI 48823, USA Tel: 5173376758
                                                                                                                                                                             Gallus
                                 USDA-ARS
                                                                                                                            Gallus gallus
Eukaryotae; Mitochondria; Metazoa; Chordata; Vertebrata; Tetrapoda;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 355)
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type=DISPERSED
14806
                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%; Score 15.4; DB 90; 76.5%; Pred. No. 7.8e+02; ive 4; Mismatches 0;
                                                H. Cheng and Oncology Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "L1MC5
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0;

repeat_region

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13449

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.4607

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primer_bind
primer_bind
BASE COUNT
ORIGIN
                                                                                               MEDLINE
REFERENCE
                                                                                                                                                                                                                               SEGMENT
SOURCE
                                                                                                                                                                                                                                                                                                                 RESULT 2:
MMHBEGFL4
LOCUS
                         FEATURES
                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                TITLE
                                                JOURNAL
                                                             TITLE
                                                                                     AUTHORS
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                                                                                                                                                                                                                     ORGANISM
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Best Local Similarity
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              source
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||:||:||:|||:|
301 TTTGAGGAAATGGATC 316
                                2 (bases 1 to 710)
Harding, P.A., Brigstock, D.R., Sher
Besner, G.E.
Direct Submission
Submitted (23-OCT-1995) Paul A. Ha
Childrens Hospital, 700 Childrens
                                                                                                        Characterization of the gene epidermal growth factor-like Gene 169 (2), 291-292 (1996) 96194822
                                                                                                                                                            1 (bases 1 to 710)
Harding, P.A., Brigstock, D.R.,
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 710)
                                                                                                                                                        Besner,
                                                                                                                                                                                                                                                                              MMHBEGFL4 710 bp DNA ROD 19-JUN-1996 Mus musculus heparin-binding epidermal growth factor-like growth factor gene, exon 5 and 6, complete cds.
                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                          4 of 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buffer:
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                                                                                                                                                                                                                              house mouse strain=129SVJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 5173376776
Email: hcheng@pilot.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             size: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Triton X-100:
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
202. .353
202. .221
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 organism="Mus"
                                                                                                                                                                                                                                                                 GI:1236398
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75.0%;
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Pred. No. 1.6e+03;
; Mismatches 0;
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48
72
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musculus"
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                                                                                                                              encoding murine heparin-binding growth factor
                                                                                Shen, L., Crissman-Combs, M.A.
                                                                                                                                                                   Shen, L.,
                                   Harding,
ens Drive,
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                                  Pediatric Columbus,
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                                  Surgery,
OH 43205,
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CNS01GZU
                                                                               COMMENT
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S Genoscope.

Direct Submission

L Submitted (16-FEB-2000) Genoscope - Centre National us provided (16-FEB-2000) Genoscope - Centre National us provided by F.H.

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

2 (bases 1 to 963)

Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

Direct Submission

Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France

This clone is from an.A. gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the

Collins and sequenced by Genoscope in collaboration with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                         Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Culicidae; Anopheles.
1 (bases 1 to 963)
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                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tagged site.
AL143803
AL143803.1 GI:7001969
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Anopheles gambiae STS T7 end of clone 07M16 of
from strain PEST of Anopheles gambiae (African
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498. .>710
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growth factor"
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growth factor"
225. .497
/note="heparin-binding epidermal growth factor-like
factor"
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/note="int
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/db_xref="taxon:10090"
/chromosome="18"
/note="129SVJ mouse genomic library in the Lambda FIX vector"
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U39191.1:155. .310,135. .207)
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/product="hepa;
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/db_xref="GI:1236400"
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75.0%;
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Pred. No. 1.7e+03;
4; Mismatches 0;
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209 TTCGAAGAAATGGATC 224
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AL439404.1
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                                                                                                        Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
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T7 end of clone BD0AA004D05 of library BD0AA from strain CBS
Candida tropicalis, sequence tagged site.
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1 (bases 1 to 997)
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Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F.
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/note="end : T7"
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/clone="07M16"
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/strain="PEST"
/organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
                                                                    Location/Qualifiers
1. .997
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75.0%;
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Pred. No. 1.8e+03;
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CNS070T9/c
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103 TTGAAGAAATGGATCC
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Wincker, P. and W
Genomic Explorat
                                                                                                                                    Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS070T9 1084 bp DNA STS 11-JAN-2001 clone AZ0AA012B01 of library AZ0AA from strain CBS 712 of Kluyveromyces marxianus, sequence tagged site.
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FEBS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B. Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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/clone_lib="BD0AA"
/note="end : T7"
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        /strain="CBS 712"
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                                                                              /organism="Kluyveromyces marxianus"
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cetales; Saccharomycetaceae; Kluyveromyces.
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Ition of the Hemiascomycetous Yeasts: 1. A set of cor molecular evolution studies(1)

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Pred. No. 1.8e+03;
4; Mismatches 0;
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Potier, S.,

. Оу BASE COUNT ORIGIN Search completed: May 15, 2001, 11:13:37 Job time: 3608 sec Ър Query Match 84.7%; Best Local Similarity 75.0%; Matches 12; Conservative 1 TTYGARGARATGGAYC 16 ||:||:||:||:||:| 426 TTCGAAGAAATGGATC 411 262 a /clone_lib="AZ0AA" 245 c 196 g Score 14.4; DB 53; Pred. No. 1.8e+03; 4; Mismatches 0; 380 t 1 others Length 1084; Indels 0; Gaps 0;